

**RAW SEQUENCE LISTING
PATENT APPLICATION US/09/016,869A**

DATE: 06/15/2000
TIME: 06:10:02

INPUT SET: S35635.raw

(A) APPLICATION NUMBER: US 08/227,371
(B) FILING DATE: 14-APR-1994

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/154,915
(B) FILING DATE: 18-NOV-1993

(viii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 07/991,997
(B) FILING DATE: 17-DEC-1992

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Vincent, Matthew P.
(B) REGISTRATION NUMBER: 36,709
(C) REFERENCE/DOCKET NUMBER: MIV-071.10

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (617) 832-1299
(B) TELEFAX: (617) 832-7000

(2) INFORMATION FOR SEQ ID NO:1:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 994 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 41..508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGAGAGGGG GAGAACAGAC AACGGGCGGC GGGGAGCAGC ATG G
Met A
1
GGG AGC AGC ATG GAG CCT TCG GCT GAC TGG CTG GCC A
Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu Ala T
87 10 15
CGG GGT CGG GTA GAG GAG GTG CGG GCG CTG CTG GAG G
Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu Glu A
90 25 30
CCC AAC GCA CCG AAT AGT TAC GGT CGG AGG CCG ATC C
Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro Ile G
93 40 45
ATG GGC AGC GCC CGA GTG GCG GAG CTG CTG CTG CTC C
Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu Leu H
96 55 60 65
CCC AAC TGC GCC GAC CCC GCC ACT CTC ACC CGA CCC G
Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro V
98 70 75 80

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/016,869A

DATE: 06/15/2000
 TIME: 06:10:03

INPUT SET: S35635.raw

100	GCC CGG GAG GGC TTC CTG GAC ACG CTG GTG CTG CAC CGG GCC GGG	343
101	Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly	
102	90 95 100	
103	GCG CGG CTG GAC GTG CGC GAT GCC TGG GGC CGT CTG CCC GTG GAC CTG	391
104	Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu	
105	105 110 115	
106	GCT GAG GAG CTG GGC CAT CGC GAT GTC GCA CGG TAC CTG CGC GCG GCT	439
107	Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg Ala Ala	
108	120 125 130	
109	GCG GGG GGC ACC AGA GGC AGT AAC CAT GCC CGC ATA GAT GCC GCG GAA	487
110	Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg Ile Asp Ala Ala Glu	
111	135 140 145	
112	GGT CCC TCA GAC ATC CCC GAT TGAAAGAACCC AGAGAGGCTC TGAGAACCT	538
113	Gly Pro Ser Asp Ile Pro Asp	
114	150 155	
115	CGGGAAACTT AGATCATCAG TCACCGAAGG TCCTACAGGG CCACAACTGC CCCCCGCCACA	598
116	ACCCACCCCG CTTTCGTAGT TTTCATTAG AAAATAGAGC TTTTAAAAAT GTCCTGCCCTT	658
117	TTAACGTAGA TATAAGCCTT CCCCCACTAC CGTAAATGTC CATTATATC ATTTTTTATA	718
118	TATTCTTATA AAAATGTAAA AAAGAAAAAC ACCGCTTCTG CCTTTTCACT GTGTTGGAGT	778
119	TTTCTGGAGT GAGCACTCAC GCCCTAAGCG CACATTATG TGCGCATTTT TTGCGAGCCT	838
120	CGCAGCCTCC GGAAGCTGTC GACTTCATGA CAAGCATTTT GTGAACTAGG GAAGCTCAGG	898
121	GGGGTTACTG GCTTCTCTTG AGTCACACTG CTAGCAAATG GCAGAACCAA AGCTCAAATA	958
122	AAAATAAAAT TATTTTCATT CATTCACTCA AAAAAAA	994

123
 124 (2) INFORMATION FOR SEQ ID NO:2:

125
 126 (i) SEQUENCE CHARACTERISTICS:
 127 (A) LENGTH: 156 amino acids
 128 (B) TYPE: amino acid
 129 (D) TOPOLOGY: linear

130
 131 (ii) MOLECULE TYPE: protein

132
 133 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

134	Met Asp Pro Ala Ala Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu	
135	1 5 10 15	
136	Ala Thr Ala Ala Ala Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu	
137	20 25 30	
138	Glu Ala Val Ala Leu Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro	
139	35 40 45	
140	Ile Gln Val Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu	
141	50 55 60	
142	Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg	
143	65 70 75 80	
144	Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val	
145	85 90 95	
146	Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg	
147	100 105 110	
148	Leu Pro Val Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg	
149	115 120 125	
150	Tyr Leu Arg Ala Ala Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg	
151	130 135 140	
152		

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/016,869A

DATE: 06/15/2000
 TIME: 06:10:04

INPUT SET: S35635.raw

153 Ile Asp Ala Ala Glu Gly Pro Ser Asp Ile Pro Asp
 154 145 150 155

155

156 (2) INFORMATION FOR SEQ ID NO:3:

157

158 (i) SEQUENCE CHARACTERISTICS:
 159 (A) LENGTH: 837 base pairs
 160 (B) TYPE: nucleic acid
 161 (C) STRANDEDNESS: single
 162 (D) TOPOLOGY: linear

163 (ii) MOLECULE TYPE: cDNA

164

165 (ix) FEATURE:
 166 (A) NAME/KEY: CDS
 167 (B) LOCATION: 328..738

168

169 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

170

171 GAGGACTCCG CGACGGTCCG CACCCTGC GG CCAGAGCGGC TTTGAGCTCG GCTGCTTCG	60
172 CGCTAGGC GC TTTTCCCAG AAGCAATCCA GGCGCGCCCG CTGGTTCTTG AGCGCCAGGA	120
173 AAAGCCCGGA GCTAACGACC GGCGCTCGG CACTGCACGG GGCCCCAAGC CGCAGAAGAA	180
174 GGACGACGGG AGGGTAATGA AGCTGAGCCC AGGTCTCTTA GGAAGGAGAG AGTGCGCCGG	240
175 AGCAGCGTGG GAAAGAAGGG AAGAGTGTG TTAAGTTTAC GGCCAACGGT GGATTATCCG	300
176 GGCGCTGCG CGTCTGGGGG CTGCGGA ATG CGC GAG GAG AAC AAG GGC ATG	351
Met Arg Glu Glu Asn Lys Gly Met	
1 5	
177 CCC AGT GGG GGC GGC AGC GAT GAG GGT CTG GCC ACG CCG GCG CGG GGA	399
Pro Ser Gly Gly Ser Asp Glu Gly Leu Ala Thr Pro Ala Arg Gly	
180 10 15 20	
181 CTA GTG GAG AAG GTG CGA CAC TCC TGG GAA GCC GGC GCG GAT CCC AAC	447
Leu Val Glu Lys Val Arg His Ser Trp Glu Ala Gly Ala Asp Pro Asn	
182 25 30 35 40	
183 GGA GTC AAC CGT TTC GGG AGG CGC GCG ATC CAG GTC ATG ATG ATG GGC	495
Gly Val Asn Arg Phe Gly Arg Arg Ala Ile Gln Val Met Met Met Gly	
184 45 50 55	
185 AGC GCC CGC GTG GCG GAG CTG CTG CTC CAC GGC GCG GAG CCC AAC	543
Ser Ala Arg Val Ala Glu Leu Leu Leu His Gly Ala Glu Pro Asn	
186 60 65 70	
187 TGC GCA GAC CCT GCC ACT CTC ACC CGA CCG GTG CAT GAT GCT GCC CGG	591
Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val His Asp Ala Ala Arg	
188 75 80 85	
189 GAG GGC TTC CTG GAC ACG CTG GTG CTG CAC CGG GCC GGG GCG CGG	639
Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly Ala Arg	
190 90 95 100	
191 CTG GAC GTG CGC GAT GCC TGG GGT CGT CTG CCC GTG GAC TTG GCC GAG	687
Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu Ala Glu	
192 105 110 115 120	
193 GAG CGG GGC CAC CGC GAC GTT GCA GGG TAC CTG CGC ACA GCC ACG GGG	735
Glu Arg Gly His Arg Asp Val Ala Gly Tyr Leu Arg Thr Ala Thr Gly	
194 125 130 135	
195 GAC TGACGCCAGG TTCCCCAGCC GCCCACAAAGC ACTTTATTTT CTTACCCAAT	788
Asp	
200 201 202 203 204 205	

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/016,869ADATE: 06/15/2000
TIME: 06:10:05

INPUT SET: S35635.raw

206 TTCCCACCCC CACCCACCTA ATTCGATGAA GGCTGCCAAC GGGGAGCGG 837
207
208 (2) INFORMATION FOR SEQ ID NO:4:
209
210 (i) SEQUENCE CHARACTERISTICS:
211 (A) LENGTH: 137 amino acids
212 (B) TYPE: amino acid
213 (D) TOPOLOGY: linear
214
215 (ii) MOLECULE TYPE: protein
216
217 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
218
219 Met Arg Glu Glu Asn Lys Gly Met Pro Ser Gly Gly Ser Asp Glu
220 1 5 10 15
221 Gly Leu Ala Thr Pro Ala Arg Gly Leu Val Glu Lys Val Arg His Ser
222 20 25 30
223 Trp Glu Ala Gly Ala Asp Pro Asn Gly Val Asn Arg Phe Gly Arg Arg
224 35 40 45
225 Ala Ile Gln Val Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu
226 50 55 60
227 Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr
228 65 70 75 80
229 Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val
230 85 90 95
231 Val Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly
232 100 105 110
233 Arg Leu Pro Val Asp Leu Ala Glu Glu Arg Gly His Arg Asp Val Ala
234 115 120 125
235 Gly Tyr Leu Arg Thr Ala Thr Gly Asp
236 130 135
237
238 (2) INFORMATION FOR SEQ ID NO:5:
239
240 (i) SEQUENCE CHARACTERISTICS:
241 (A) LENGTH: 853 base pairs
242 (B) TYPE: nucleic acid
243 (C) STRANDEDNESS: both
244 (D) TOPOLOGY: linear
245
246 (ii) MOLECULE TYPE: cDNA
247
248 (ix) FEATURE:
249 (A) NAME/KEY: CDS
250 (B) LOCATION: 213..587
251
252 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
253
254 GGAGTACAGC AGCGGGAGCA TGGGTGCGAG GTTCTTGTC ACTGTAAGGA TTCAGCGCGC 60
255
256 GGGCCGCCA CTCCAAGAGA GGGTTTTCTT GGTGAAGTTC GTGCGATCCC GGAGACCCAG 120
257
258 GACAGCGAGC TGCGCTCTGG CTTTCGTGAA CATGTTGTTG AGGCTAGAGA GGATCTTGAG 180

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION **US/09/016,869A**

DATE: 06/15/2000
TIME: 06:10:06

INPUT SET: S35635.raw

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Original Text